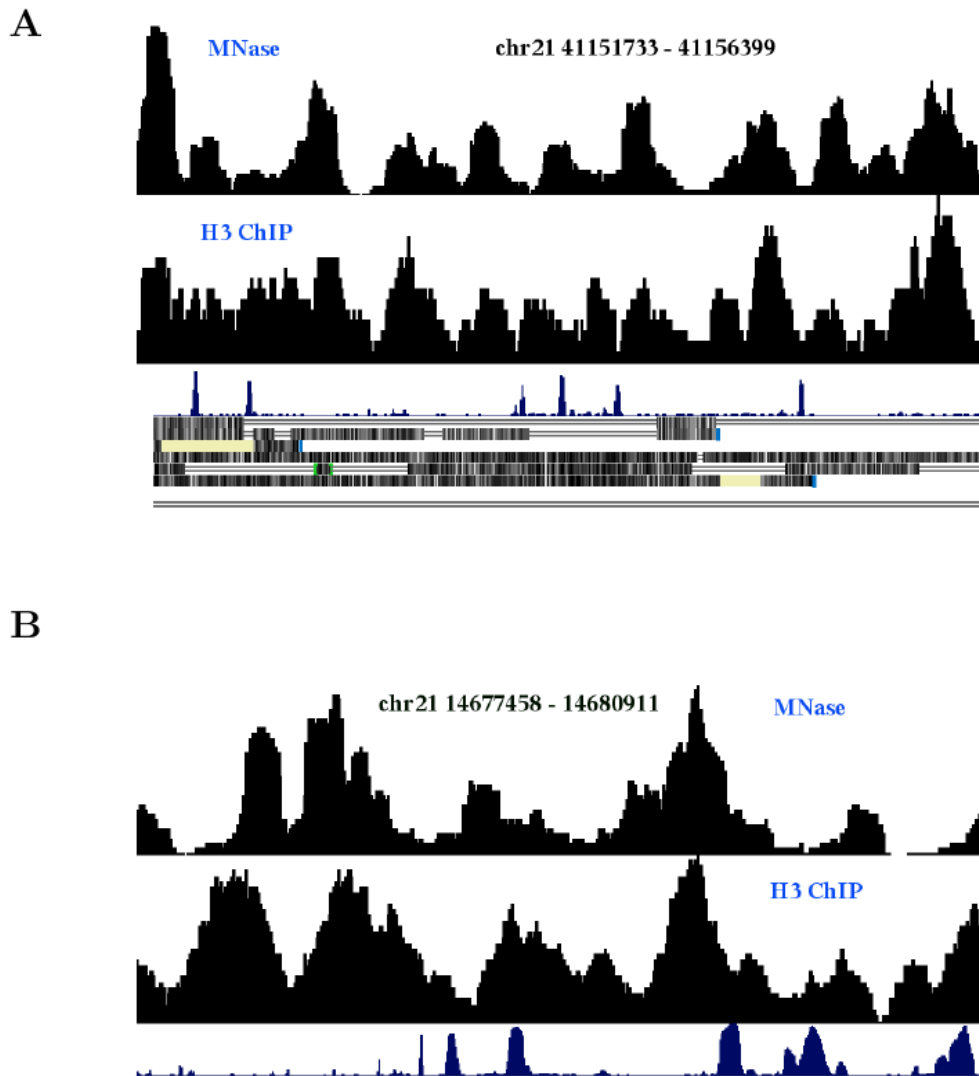


## Supplemental Data

### Dynamic Regulation of Nucleosome

#### Positioning in the Human Genome

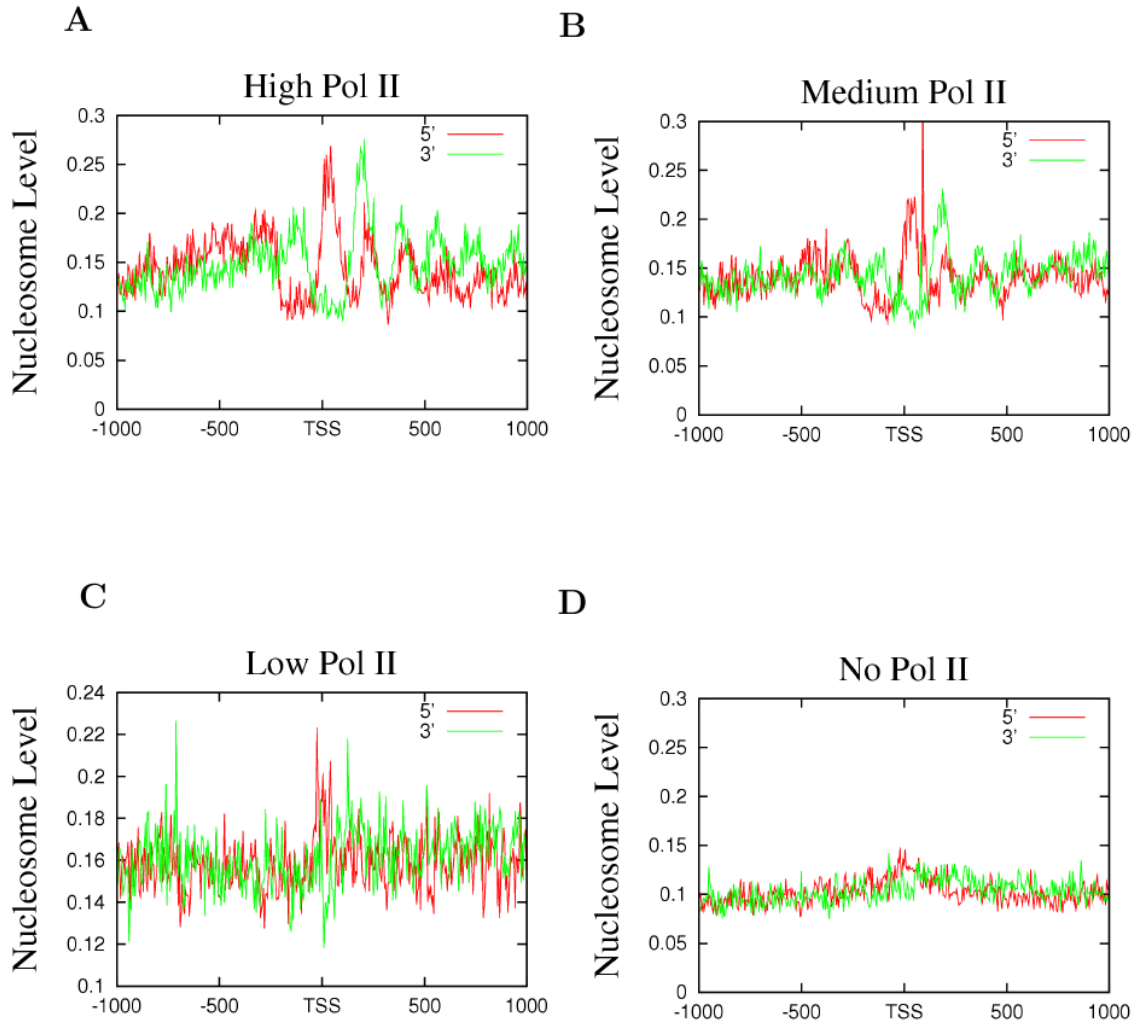
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**Figure S1. Correspondence of nucleosome distribution obtained using MNase digestion and histone distribution obtained using ChIP-Seq with a histone H3 antibody.**

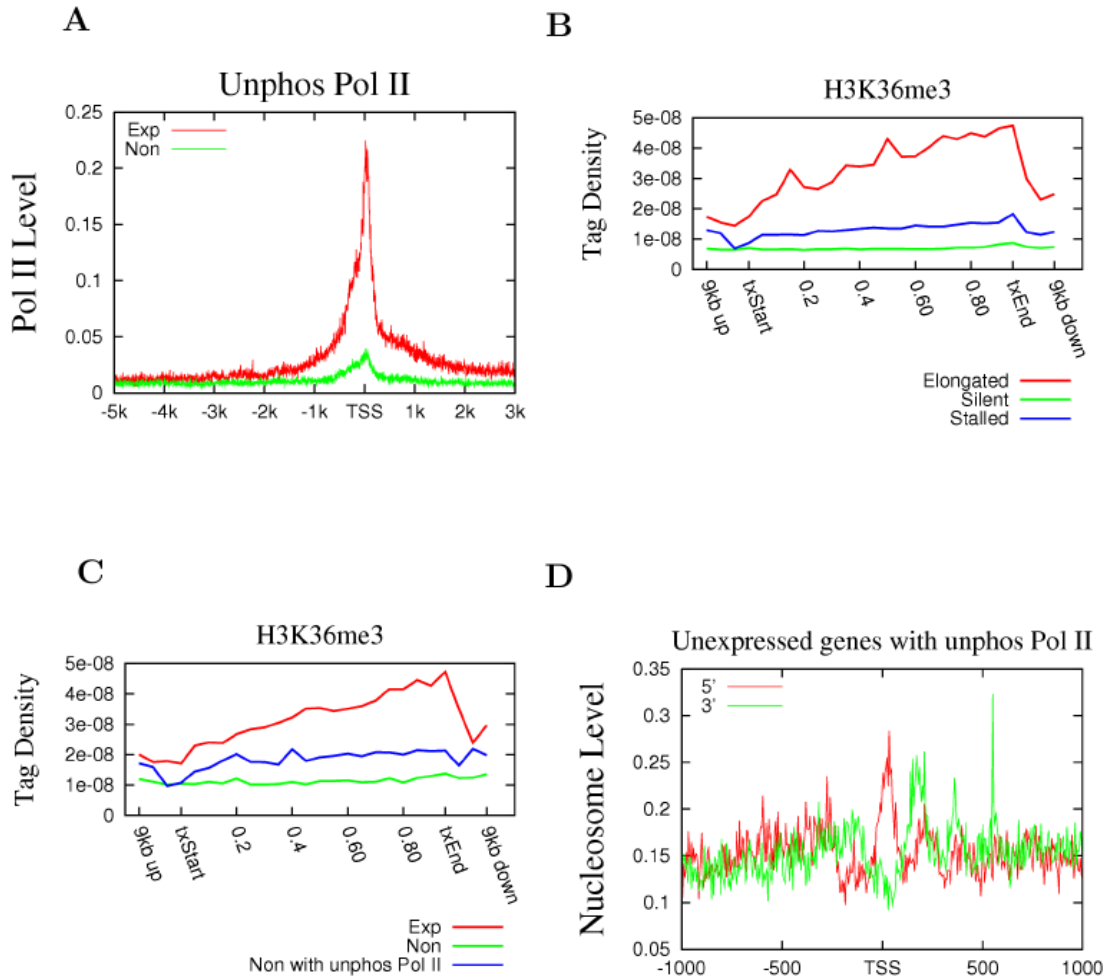
Nucleosome profiles were generated as described in Experimental Procedures, with the exception that both of the profiles were generated with larger window sizes. Specifically, scores were generated by sliding 10 bp windows with all reads mapping to the sense strand 150 bp upstream of the window contributing and all reads mapping to the antisense strand 150 bp downstream of the window contributing.

- A.** Correspondence for a ~ 4.6 kb region at chr21 41151733 – 41156399.
- B.** Correspondence for a ~ 3.5 kb region at chr21 14677458 – 14680911.



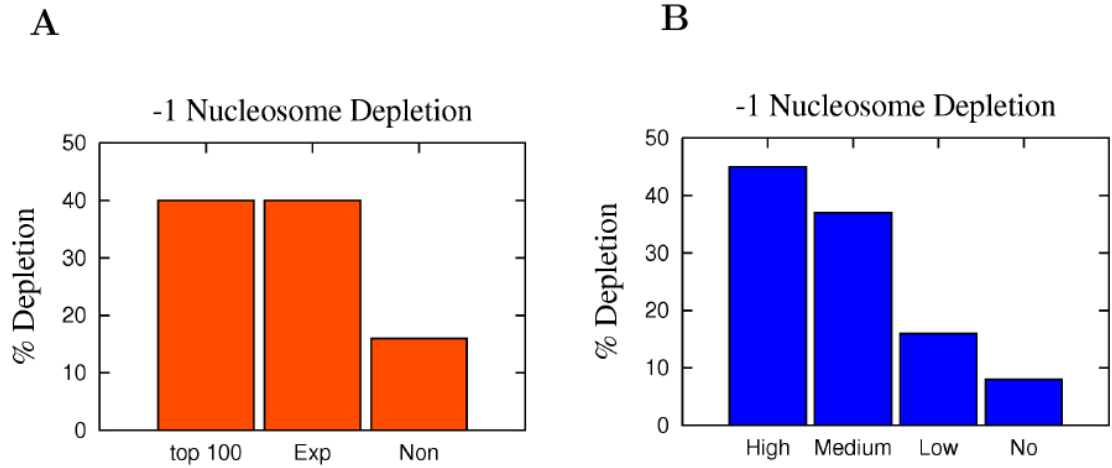
**Figure S2. Nucleosome phasing near TSSs in relation to Pol II levels in promoter regions.**

The y-axis shows the number of sequence tags from the sense strand (red) and antisense strand (green) of DNA at each position 1 kb upstream to 1 kb downstream of the TSS for genes with (A) high levels of promoter Pol II, (B) medium levels of promoter Pol II, (C) low levels of promoter Pol II and (D) promoters with no Pol II signal.



**Figure S3. Using unphosphorylated Pol II to define genes with stalled Pol II.**

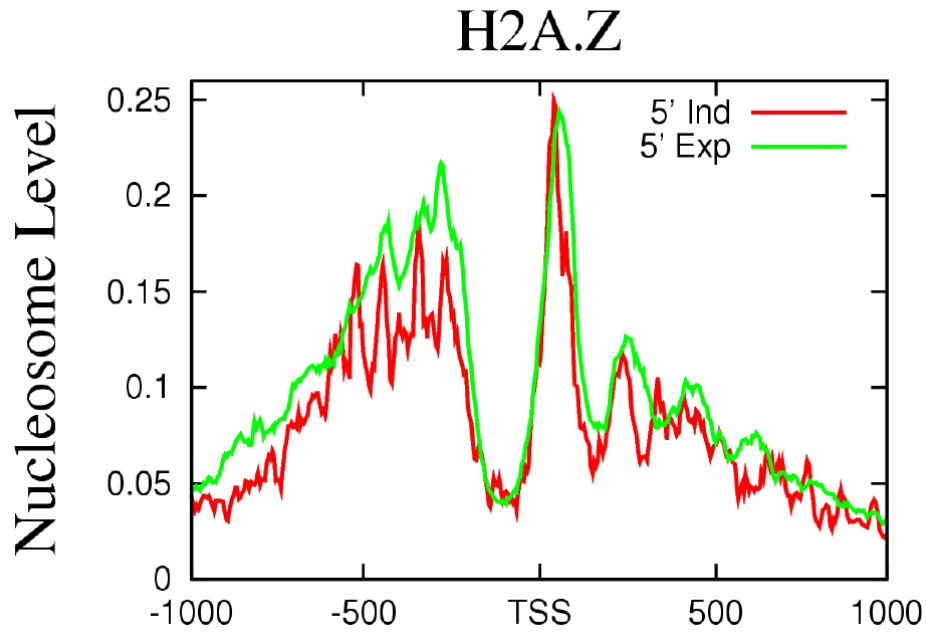
- A.** The distribution of unphosphorylated Pol II across promoter regions for expressed (Exp) and unexpressed (Non) genes.
- B.** H3K36me3 tag density (see Experimental Procedures for details) across genes defined as having Elongated, Silent or Stalled Pol II (see Experimental Procedures for definitions).
- C.** H3K36me3 tag density across genes that are expressed (Exp), unexpressed (Non) and classified as stalled by having significant levels of unphosphorylated Pol II and no detectable transcription.
- D.** Nucleosome organization near the TSS of genes defined as stalled by having significant levels of unphosphorylated Pol II and no detectable transcription.



**Figure S4. Nucleosome depletion at the -1 nucleosome position in relation to mRNA expression level and promoter polymerase II level.**

**A.** The percentage of the -1 nucleosome depletion relative to the -2 nucleosome for the 100 genes with the highest mRNA expression levels, all expressed genes and all non-expressed genes.

**B.** The percentage of the -1 nucleosome depletion relative to the -2 nucleosome for gene sets with high, medium, low and no promoter Pol II signals. The gene sets here are the same as those in Figure S2.



**Figure S5. H2A.Z nucleosomes are preferentially removed from the -1 nucleosome position in the TCR-inducible genes in resting CD4<sup>+</sup> T cells.**

**Table S1. Unique tag numbers for sequenced libraries**

<b>Library</b>	<b>Cell Type</b>	<b>Unique Read Number</b>
Nucleosome	Resting	154582677
Histone H3	Resting	75066295
Unphosphorylated Pol II	Resting	4669495
Ser5 phosphorylated Pol II	Resting	5271481
Nucleosome	Activated	141931997
Unphosphorylated Pol II	Activated	4523455
Ser5 phosphorylated Pol II	Activated	5101490